FILE 'EMBASE' ENTERED AT 15:31:55 ON 24 FEB 2004

FILE 'BIOSIS' ENTERED AT 15:31:55 ON 24 FEB 2004

=> s (uricase or urate oxidase) and non-tetrameric aggregates
L13 0 (URICASE OR URATE OXIDASE) AND NON-TETRAMERIC AGGREGATES

=> s (uricase or urate oxidase) and (dimer or monomer)
L14 10 (URICASE OR URATE OXIDASE) AND (DIMER OR MONOMER)

=> dup rem l14
PROCESSING COMPLETED FOR L14
L15 5 DUP REM L14 (5 DUPLICATES REMOVED)

=> d l15 1-5 ibib ab

L15 ANSWER 1 OF 5 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2002453400 MEDLINE Full-text
DOCUMENT NUMBER: 22197991 PubMed ID: 12208494
TITLE: Towards a new T-fold protein?: the coproporphyrinogen III oxidase sequence matches many structural features from **urate oxidase.**
AUTHOR: Colloc'h Nathalie; Mornon Jean-Paul; Camadro Jean-Michael
CORPORATE SOURCE: Universite de Caen, CNRS UMR6551, bd. Henri Becquerel, BP5229, 14074 Caen Cedex, France.. n.colloch@neuro.unicaen.fr
SOURCE: FEBS LETTERS, (2002 Aug 28) 526 (1-3) 5-10. Journal code: 0155157. ISSN: 0014-5793.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200210
ENTRY DATE: Entered STN: 20020906
Last Updated on STN: 20021018
Entered Medline: 20021017

AB **Urate oxidase** (UOX) and coproporphyrinogen III oxidase (CPO) are two unusual oxidases as they accomplish their catalytic act with no co-factor nor metal ion. They both require molecular oxygen, and lead to hydrogen peroxide in addition to the product. UOX is composed of two contiguous Tunneling-fold domains and CPO appears to be also divided into two structurally equivalent domains. Moreover, each of these putative domains can be coherently aligned on UOX domains. Although their sequences are very distant, we therefore suggest that functional CPO **dimer** is built around a tunnel, with the substrate sitting above it, on the N- and C-terminal side. This overall model is supported by mutation data and is coherent with the chemical events expected for substrate processing by CPO.

L15 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:380137 CAPLUS Full-text
DOCUMENT NUMBER: 131:155288
TITLE: Crystal structure of 7,8-dihydroneopterin triphosphate epimerase
AUTHOR(S): Ploom, Tarmo; Haussmann, Christoph; Hof, Peter; Steinbacher, Stefan; Bacher, Adelbert; Richardson, John; Huber, Robert
CORPORATE SOURCE: Max-Planck-Institut fur Biochemie, Abteilung

Strukturforschung, Martinsried, D-82152, Germany
SOURCE: Structure (London) (1999), 7(5), 509-516
CODEN: STRUE6; ISSN: 0969-2126
PUBLISHER: Current Biology Publications
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Dihydroneopterin triphosphate (H2NTP) is the central substrate in the biosynthesis of folate and tetrahydrobiopterin. Folate serves as a cofactor in amino acid and purine biosynthesis and tetrahydrobiopterin is used as a cofactor in amino acid hydroxylation and NO synthesis. In bacteria, H2NTP enters the folate biosynthetic pathway after nonenzymic dephosphorylation; in vertebrates, H2NTP is used to synthesize tetrahydrobiopterin. Dihydroneopterin triphosphate epimerase (I) of Escherichia coli catalyzes the inversion of C2' of H2NTP. Here, the crystal structure of the E. coli homo-octameric protein was solved by a combination of multiple isomorphous replacement, Patterson search techniques, and cyclic averaging, and was refined to a crystallog. R factor of 18.8% at 2.9 Å resolution I was found to be a torus-shaped, D4 sym. homo-octamer with approx. dimensions of 65 + 65 Å. Four I monomers formed an unusual 16-stranded antiparallel β barrel by tight association between the N- and C-terminal β strands of 2 adjacent subunits. Two tetramers associated in a head-to-head fashion to form the active enzyme complex. The folding topol., quaternary structure and amino acid sequence of I was similar to that of dihydroneopterin aldolase involved in the biosynthesis of folic acid. The **monomer** fold of I was also topol. similar to that of GTP cyclohydrolase I, 6-pyrovoyltetrahydropterin synthase, and **urate oxidase** (UO). Despite a lack of significant sequence homol., these proteins share a common subunit fold and oligomerize to form central β-barrel structures employing different cyclic symmetry elements, D4, D5, D3, and D2, resp. Moreover, these enzymes have a topol. equivalent acceptor site for the 2-amino-4-oxo pyrimidine (2-oxo-4-oxo pyrimidine in UO) moiety of their resp. substrates.

REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 3 OF 5 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 84051215 MEDLINE Full-text
DOCUMENT NUMBER: 84051215 PubMed ID: 6685457
TITLE: **Uricase** from soybean root nodules: purification, properties, and comparison with the enzyme from cowpea.
AUTHOR: Lucas K; Boland M J; Schubert K R
SOURCE: ARCHIVES OF BIOCHEMISTRY AND BIOPHYSICS, (1983 Oct 1) 226 (1) 190-7.
Journal code: 0372430. ISSN: 0003-9861.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198312
ENTRY DATE: Entered STN: 19900319
Last Updated on STN: 19970203
Entered Medline: 19831217

AB A 45-fold purification of **uricase** (urate:O2 oxidoreductase, EC 1.7.3.3) from soybean root nodules by ammonium sulfate fractionation, gel filtration, and affinity chromatography is described. Electrophoresis on nondenaturing gels using an activity stain or on sodium dodecyl sulfate (SDS) gels demonstrated that the enzyme obtained was nearly homogeneous. The subunit molecular weight of **uricase** estimated from SDS gels was 32,000 +/- 3000. Gel-filtration studies indicated that the native enzyme is a **monomer** at pH 7.5 which associates to form a **dimer** at pH 8.8. Enzyme activity was stabilized by the

addition of dithiothreitol. The pH dependence of the enzyme showed an optimum of 9.5. Initial rate kinetics showed Km values of 10 and 31 microM for uric acid and oxygen, respectively, with an intersecting pattern of substrate dependence. **Uricase** activity was inhibited strongly by xanthine, which was competitive with respect to uric acid (Ki = 10 microM). No significant inhibition was observed in the presence of a variety of amino acids, ammonium, adenine, or allopurinol, in contrast with results reported for the cowpea enzyme. Gel-filtration chromatography and SDS-gel electrophoresis of **uricase** purified by the same method from cowpea nodules indicated that the native enzyme exists as a **monomer** of Mr 50,000 at pH 7.5.

L15 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1974:11923 CAPLUS Full-text
DOCUMENT NUMBER: 80:11923
TITLE: Water-insoluble enzyme compositions
INVENTOR(S): Chibata, Ichiro; Tosa, Tetsuya; Mori, Takao
PATENT ASSIGNEE(S): Tanabe Seiyaku Co., Ltd.
SOURCE: Ger. Offen., 30 pp.
CODEN: GWXXBX
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
DE 2252888	A1	19730719	DE 1972-2252888	19721027
JP 48049680	A2	19730713	JP 1971-85776	19711028
JP 52018271	B4	19770520		
JP 49042878	A2	19740422	JP 1972-89879	19720907
JP 52018791	B4	19770524		
JP 49042880	A2	19740422	JP 1972-89883	19720907
JP 52018792	B4	19770524		
JP 49042881	A2	19740422	JP 1972-89884	19720907
JP 52018793	B4	19770524		

PRIORITY APPLN. INFO.:
JP 1971-85776 19711028
JP 1972-89879 19720907
JP 1972-89883 19720907
JP 1972-89884 19720907

AB The enzymes, urease, **uricase**, asparaginase, and aspartase, were insolubilized by either immobilizing in the lattice of a polymer of an acrylamide **monomer** (acrylamide, N,N'-methylene-bis-acrylamide or N,N'-propylene-bis-acrylamide) or by emulsification in an aqueous solvent containing the enzyme, a polyamino compound (hexamethylene diamine, triethylene diamine) and a hydrophobic solvent, and subsequent addition of a polybasic acid halogenide (sebacoyl halogenide, terephthaloyl halogenide, adipoyl halogenide) or of a polycyanate compound (toluyl diisocyanate or hexamethylene diisocyanate).

L15 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1971:532983 CAPLUS Full-text
DOCUMENT NUMBER: 75:132983
TITLE: **Uricase** stabilization
INVENTOR(S): Nakagiri, Yoshitaka; Kihara, Riichiro
PATENT ASSIGNEE(S): Toyo Spinning Co., Ltd.
SOURCE: Jpn. Tokkyo Koho, 3 pp.
CODEN: JAXXAD
DOCUMENT TYPE: Patent
LANGUAGE: Japanese

FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 46029785	B4	19710830	JP	19680709

AB **Uricase** is stabilized or reactivated by reducing agents, e.g. Na hydrosulfite, ascorbic acid, NaBH4, Na2S, or Na2SO3. Gel filtration paterns indicated reduction of the **uricase dimer.**

=> log y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
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DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
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NEWS 4	DEC 08	INPADOC: Legal Status data reloaded
NEWS 5	SEP 29	DISSABS now available on STN
NEWS 6	OCT 10	PCTFULL: Two new display fields added
NEWS 7	OCT 21	BIOSIS file reloaded and enhanced
NEWS 8	OCT 28	BIOSIS file segment of TOXCENTER reloaded and enhanced
NEWS 9	NOV 24	MSDS-CCOHS file reloaded
NEWS 10	DEC 08	CABA reloaded with left truncation
NEWS 11	DEC 08	IMS file names changed
NEWS 12	DEC 09	Experimental property data collected by CAS now available in REGISTRY
NEWS 13	DEC 09	STN Entry Date available for display in REGISTRY and CA/CAplus
NEWS 14	DEC 17	DGENE: Two new display fields added
NEWS 15	DEC 18	BIOTECHNO no longer updated
NEWS 16	DEC 19	CROPU no longer updated; subscriber discount no longer available

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 NEWS 17  DEC 22  Additional INPI reactions and pre-1907 documents added to CAS
                  databases
 NEWS 18  DEC 22  IFIPAT/IFIUDB/IFICDB reloaded with new data and search fields
 NEWS 19  DEC 22  ABI-INFORM now available on STN
 NEWS 20  JAN 27  Source of Registration (SR) information in REGISTRY updated
                  and searchable
 NEWS 21  JAN 27  A new search aid, the Company Name Thesaurus, available in
                  CA/CAplus
 NEWS 22  FEB 05  German (DE) application and patent publication number format
                  changes

 NEWS EXPRESS  DECEMBER 28 CURRENT WINDOWS VERSION IS V7.00, CURRENT
               MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
               AND CURRENT DISCOVER FILE IS DATED 23 SEPTEMBER 2003
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=> s alvares k/au
L1          35 ALVARES K/AU

=> s l1 and urate oxidase
L2           7 L1 AND URATE OXIDASE

=> dup rem l1
PROCESSING COMPLETED FOR L1
L3          32 DUP REM L1 (3 DUPLICATES REMOVED)

=> dup rem l2
PROCESSING COMPLETED FOR L2
L4           7 DUP REM L2 (0 DUPLICATES REMOVED)

=> d l4 1-7 ibib ab
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L4 ANSWER 1 OF 7 MEDLINE on STN
ACCESSION NUMBER: 94216348 MEDLINE Full-text
DOCUMENT NUMBER: 94216348 PubMed ID: 8163532
TITLE: Amphibian allantoinase. Molecular cloning, tissue distribution, and functional expression.
AUTHOR: Hayashi S; Jain S; Chu R; **Alvares K**; Xu B; Erfurth F; Usuda N; Rao M S; Reddy S K; Noguchi T; +
CORPORATE SOURCE: Department of Pathology, Northwestern University Medical School, Chicago, Illinois 60611.
CONTRACT NUMBER: R37 GM23750 (NIGMS)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1994 Apr 22) 269 (16) 12269-76.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U03471
ENTRY MONTH: 199405
ENTRY DATE: Entered STN: 19940606
Last Updated on STN: 19970203
Entered Medline: 19940526

AB The chain of enzymes necessary to convert uric acid to its metabolic products urea and glyoxylic acid in vertebrates is truncated through the successive loss of allantoicase, allantoinase, and **urate oxidase** during phylogenetic evolution. Previous studies have assigned the localization of both **urate oxidase** and allantinase to the peroxisome in the amphibian liver. This study reports the cloning of a cDNA encoding bullfrog (Rana catesbeiana) allantoinase, an enzyme that converts allantoin to allantoic acid. The cDNA is 2112 base pairs in length containing a 1449-base pair open reading frame which corresponds to a 483-residue protein (53,296 Da). Structural analysis of the deduced protein suggested two potential transmembrane segments and the presence of a putative mitochondrial localization sequence in the amino terminus. Immunocytochemical analysis revealed that allantoinase is localized to mitochondria and not to peroxisomes. On Northern blotting, a single mRNA species was detected in the liver and kidney of frog but not in other tissues; this distribution was confirmed by immunoblotting. The hepatic- and renal-specific expression of allantoinase coincides with the distribution of **urate oxidase** in these tissues in the frog. The allantoinase expressed in Saccharomyces cerevisiae and in Spodoptera frugiperda (Sf9) insect cells exhibits catalytic activity and is antigenically identical to the native frog enzyme.

L4 ANSWER 2 OF 7 MEDLINE on STN
ACCESSION NUMBER: 94334372 MEDLINE Full-text
DOCUMENT NUMBER: 94334372 PubMed ID: 8056832
TITLE: Uric acid degrading enzymes, **urate oxidase** and allantoinase, are associated with different subcellular organelles in frog liver and kidney.
AUTHOR: Usuda N; Hayashi S; Fujiwara S; Noguchi T; Nagata T; Rao M S; **Alvares K**; Reddy J K; Yeldandi A V
CORPORATE SOURCE: Department of Pathology, Northwestern University Medical School, Chicago, Illinois 60611.
CONTRACT NUMBER: R37 GM23750 (NIGMS)
SOURCE: JOURNAL OF CELL SCIENCE, (1994 Apr) 107 (Pt 4) 1073-81.
Journal code: 0052457. ISSN: 0021-9533.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199409
ENTRY DATE: Entered STN: 19940920
Last Updated on STN: 19940920
Entered Medline: 19940913

AB On the basis of differential and density gradient centrifugation studies, the site of the uric acid degrading enzymes, **urate oxidase** and allantoinase, in amphibia was previously assigned to the hepatic peroxisomes. Using specific antibodies against frog **urate oxidase** and allantoinase, we have undertaken an immunocytochemical study of the localization of these two proteins in frog liver and kidney, and demonstrate that whereas **urate oxidase** is present in peroxisomes, allantoinase is localized in mitochondria. **Urate oxidase** and allantoinase were detected by immunoblot analysis in both frog liver and kidney. The subcellular localization of these two enzymes was ascertained by Protein A-gold immunocytochemical staining of Lowicryl K4M-embedded tissue. Peroxisomes in frog liver parenchymal cells and kidney proximal tubular epithelium contained a semi-dense subcrystalloid core, which was found to be the exclusive site of **urate oxidase** localization. Allantoinase was detected within mitochondria, but not in peroxisomes of hepatocytes or proximal tubular epithelium. No allantoinase was detected in the mitochondria of nonhepatic parenchymal cells in liver and of the cells lining the distal convoluted tubules of the kidney. These results demonstrate that, unlike rat kidney peroxisomes which lack **urate oxidase**, peroxisomes of frog kidney contain this enzyme. Contrary to previous assumptions, these studies also clearly establish that **urate oxidase** and allantoinase, the first two enzymes involved in uric acid degradation, are localized in different subcellular organelles in frog liver and kidney.

L4 ANSWER 3 OF 7 MEDLINE on STN
ACCESSION NUMBER: 92279236 MEDLINE Full-text
DOCUMENT NUMBER: 92279236 PubMed ID: 1594592
TITLE: Rat **urate oxidase** produced by recombinant baculovirus expression: formation of peroxisome crystalloid core-like structures.
AUTHOR: **Alvares K**; Widrow R J; Abu-Jawdeh G M; Schmidt J V; Yeldandi A V; Rao M S; Reddy J K
CORPORATE SOURCE: Department of Pathology, Northwestern University Medical School, Chicago, IL 60611.
CONTRACT NUMBER: R37GM23750 (NIGMS)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1992 Jun 1) 89 (11) 4908-12.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199206
ENTRY DATE: Entered STN: 19920710
Last Updated on STN: 19920710
Entered Medline: 19920626

AB **Urate oxidase** (EC 1.7.3.3), which catalyzes the oxidation of uric acid to allantoin, is present in most mammals but absent in humans and hominoid primates. In rats and most other mammals that catabolize uric acid to allantoin, this enzyme is localized within the crystalloid cores of peroxisomes present in liver parenchymal cells. To determine whether **urate oxidase** forms these crystalloid cores or whether core-forming protein(s) exist in association with **urate oxidase**, a baculovirus expression vector system was used to overproduce the full-length rat **urate oxidase** in Spodoptera frugiperda

cells. **Urate oxidase** was expressed to a level of approximately 30% of the total protein in this system. Immunoblot analysis demonstrated that the baculovirus-generated protein had electrophoretic and immunologic properties similar to those of **urate oxidase** expressed in rat liver. Immunofluorescence and electron microscopic examination revealed that the overexpressed recombinant **urate oxidase** is present in both the cytoplasm and the nucleus of infected insect cells as numerous 1- to 3-microns discrete particles. These insoluble protein aggregates, which were positively stained for **urate oxidase** by protein A-gold immunocytochemical approach, did not appear to be delimited by a single membrane. They revealed a crystalloid structure reminiscent of rat peroxisomal core consisting of bundles of tubules with an inner diameter of approximately 50 A. The recombinant **urate oxidase** particles, isolated by a single-step procedure, were composed entirely of 35-kDa **urate oxidase** subunit. These studies indicate that rat **urate oxidase** is capable of forming insoluble crystalloid core-like structures.

L4 ANSWER 4 OF 7 MEDLINE on STN
ACCESSION NUMBER: 92112056 MEDLINE Full-text
DOCUMENT NUMBER: 92112056 PubMed ID: 1765273
TITLE: Molecular evolution of the **urate oxidase** -encoding gene in hominoid primates: nonsense mutations.
AUTHOR: Yeldandi A V; Yeldandi V; Kumar S;.Murthy C V; Wang X D; **Alvares K**; Rao M S; Reddy J K
CORPORATE SOURCE: Department of Pathology, Northwestern University Medical School, Chicago, IL 60611.
CONTRACT NUMBER: R37 GM23750 (NIGMS)
SOURCE: GENE, (1991 Dec 30) 109 (2) 281-4.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M69165; GENBANK-M69166; GENBANK-M69167; GENBANK-M69168; GENBANK-M69169; GENBANK-M69170; GENBANK-M69171; GENBANK-M69172; GENBANK-M69173; GENBANK-M69174
ENTRY MONTH: 199202
ENTRY DATE: Entered STN: 19920308
Last Updated on STN: 19920308
Entered Medline: 19920218

AB Nucleotide sequences of portions of second and fifth exons of **urate oxidase** encoding gene (UOX) of chimpanzee, gorilla, orangutan, rhesus monkey and squirrel monkey obtained following amplification by polymerase chain reaction have been compared with corresponding sequences of human, baboon and rat UOX. Two or more nonsense mutations are found in the coding regions of this UOX gene thus far analyzed in human, chimpanzee, gorilla and orangutan, but not in the baboon, rhesus monkey and squirrel monkey. Of these nonsense mutations, the stop codon at amino acid position 33 is constant in the human and the three great apes suggesting that this may be the original mutation responsible for the inactivation of the UOX gene during hominoid evolution.

L4 ANSWER 5 OF 7 MEDLINE on STN
ACCESSION NUMBER: 91153651 MEDLINE Full-text
DOCUMENT NUMBER: 91153651 PubMed ID: 1999285
TITLE: Rat **urate oxidase**: cloning and structural analysis of the gene and 5'-flanking region.
AUTHOR: Wang X D; Kawano H; **Alvares K**; Reddy P G; Getto H; Rao M S; Reddy J K

CORPORATE SOURCE: Department of Pathology, Northwestern University Medical School, Chicago, IL 60611.
CONTRACT NUMBER: R 37 GM23750 (NIGMS)
SOURCE: GENE, (1991 Jan 15) 97 (2) 223-9.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M30287; GENBANK-M30288; GENBANK-M30289; GENBANK-M30290; GENBANK-M30291; GENBANK-M30292; GENBANK-M30293; GENBANK-M30294; GENBANK-M63583; GENBANK-M63586; GENBANK-M63587; GENBANK-M63588; GENBANK-M63590; GENBANK-M63591; GENBANK-M63592; GENBANK-M63593; GENBANK-S75876; GENBANK-S75878
ENTRY MONTH: 199104
ENTRY DATE: Entered STN: 19910428
Last Updated on STN: 19910428
Entered Medline: 19910408

AB The structural gene (UOX) encoding rat **urate oxidase** (UOX) spans at least 23 kb and is composed of eight exons and seven introns. All of the exon-intron splice junction sequences conformed to the GT/AG consensus established for eukaryotic genes. The transcription start point (tsp) was determined using S1-type nuclease protection riboprobe, and assigned to an adenine 54 nucleotides (nt) upstream of the ATG start codon. A 456-bp 5'-terminal fragment, starting at the ATG codon, carries a putative TATA (ATAAAA) sequence at -32, and two putative 'CAAT box' sequences at -62 and -71 bp upstream from the tsp. No sequence resembling 'GC' box hexanucleotides (GGGCGG or CCGCCC) was found. The structural features of the 5'-flanking region of the UOX gene are distinct from the 5'-flanking sequences of peroxisomal beta-oxidation system genes which contain one or more 'GC' box elements but lack TATA- and CAAT-like features [Osumi et al., J. Biol. Chemical 262 (1987) 8138-8143; Ishii et al., J. Biol. Chemical 262 (1987) 8144-8150]. The 5'-flanking region of the UOX gene reveals a sequence, TTAGTAATT at nt -276 from the tsp, which appears to be complementary to the underlined part of the liver-specific LF-B1/HNF-1 consensus sequence, GTTAATNATTAAC (where N = A, C, T, G or no nt).

L4 ANSWER 6 OF 7 MEDLINE on STN
ACCESSION NUMBER: 90386634 MEDLINE Full-text
DOCUMENT NUMBER: 90386634 PubMed ID: 2403354
TITLE: Human **urate oxidase** gene: cloning and partial sequence analysis reveal a stop codon within the fifth exon.
AUTHOR: Yeldandi A V; Wang X D; **Alvares K**; Kumar S; Rao M S; Reddy J K
CORPORATE SOURCE: Department of Pathology, Northwestern University Medical School, Chicago, IL 60611.
CONTRACT NUMBER: R37 GM23750 (NIGMS)
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1990 Sep 14) 171 (2) 641-6.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M30291; GENBANK-M30292; GENBANK-M30293; GENBANK-M30294
ENTRY MONTH: 199010
ENTRY DATE: Entered STN: 19901122

Last Updated on STN: 19901122
Entered Medline: 19901019

AB Using the cDNA and selected genomic probes of rat **urate oxidase**, we have screened the human genomic library and isolated seven clones; one clone (clone 13) contained exonic regions which correspond to the exons 5, 6, and 7 of rat **urate oxidase** gene. The nucleotide sequence was determined for these three exons and exon/intron junctions, and compared with the sequence from the rat gene. A mutation resulting in a stop codon TGA was found in the fifth exon of the human **urate oxidase** gene. Sequence analysis of the polymerase chain reaction amplified DNA, corresponding to the fifth exon of **urate oxidase** from DNA samples from four different individuals, confirmed the same TGA stop codon in all. This single stop codon mutation and/or other mutation(s) in this gene may be responsible for the lack of **urate oxidase** activity in the human.

L4 ANSWER 7 OF 7 MEDLINE on STN
ACCESSION NUMBER: 89149825 MEDLINE Full-text
DOCUMENT NUMBER: 89149825 PubMed ID: 2920046
TITLE: The nucleotide sequence of a full length cDNA clone encoding rat liver **urate oxidase.**
AUTHOR: **Alvares K**; Nemali M R; Reddy P G; Wang X D; Rao M S; Reddy J K
CORPORATE SOURCE: Department of Pathology, Northwestern University Medical School, Chicago, Illinois 60611.
CONTRACT NUMBER: R37 GM 23750 (NIGMS)
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS (1989 Feb 15) 158 (3) 991-5.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M24396
ENTRY MONTH: 198904
ENTRY DATE: Entered STN: 19900306
Last Updated on STN: 19970203
Entered Medline: 19890403

AB Recently we reported the sequence of a cDNA clone (pUOX-1), isolated from a lambda gt11 cDNA library, which encoded for rat liver **urate oxidase** (EC 1.7.3.3), but this clone lacked the nucleotide sequences encoding the N-terminal region for this enzyme. Using the cDNA insert from the pUOX-1 clone as a probe, we have now isolated a full length cDNA clone, pUOX-2, from a lambda gt10 library by plaque hybridization. Nucleotide sequence analysis of the pUOX-2 clone showed that it has 1379 base pairs with an open reading frame coding for 303 amino acid residues corresponding to a molecular mass of 34,931 daltons. In addition to the open reading frame the pUOX-2 contains 439 bp of 3'-untranslated and 41 bp of 5'-untranslated sequences. The consensus polyadenylation signal AATAAA precedes a stretch of poly(A)+ residues at the 3' end.

=> log y
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